

**Fig. S1. Phylogeny of Actinopterygian HIF $\alpha$  reconstructed by Bayesian inference using full-length CDS.** Evolutionary analyses were conducted in BEAST 2 (v2.6.1) using the General Time Reversible model (GTR) with 6 gamma categories (+G) and allowing for invariants (+I). The tree with maximum clade credibility and mean heights is shown with posterior probability values next to the branches. The highest tree likelihood was -41437.47 with an ESS of 587. The tree was re-rooted on the outgroup for visualization. Four HIF $\alpha$  homology groups are indicated to the right and the following taxa are color coded within each group: Otocephala (green); Salmoniformes (orange); Neoteleostei (blue). The outgroup, *Ciona intestinalis*, basal Actinopterygian (spotted gar, *Lepisosteus oculatus*), basal teleost (Asian arowana, *Scleropages formosus*), and sister taxa to Salmoniformes (Northern pike, *Esox lucius*), are not color coded. Sequences are identified by the first letter of the genus and species followed by the last four digits of the NCBI or Ensemble reference gene accession number (see supplementary table S1, Supplementary Material online for a full list of genes). **NOTE:** this is a rectangular representation of the tree as shown in fig. 1 in circular format.

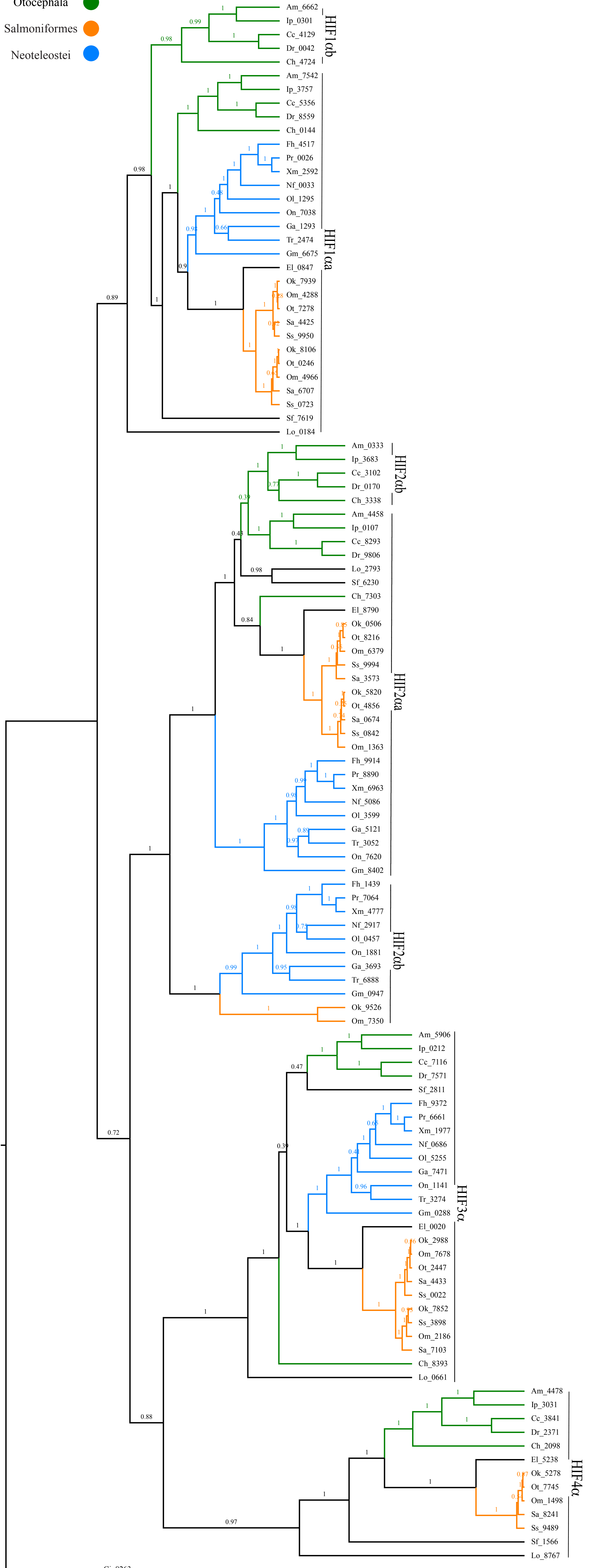
**Fig. S2. Phylogeny of Actinopterygian HIF $\alpha$  reconstructed by maximum likelihood using full-length CDS.** Evolutionary analyses were conducted in MEGAX (v10.1.8) using the General Time Reversible model (GTR) with 6 gamma categories(+G) and allowing for invariants (+I). The tree with the highest log likelihood (-41489.7) is shown with bootstrap values next to the branches. The tree was re-rooted on the outgroup for visualization. Four HIF $\alpha$  homology groups are indicated to the right and the following taxa are color coded within each group: Otocephala (green); Salmoniformes (orange); Neoteleostei (blue). The outgroup, *Ciona intestinalis*, basal Actinopterygian (spotted gar, *Lepisosteus oculatus*), basal teleost (Asian arowana, *Scleropages formosus*), and sister taxa to Salmoniformes (Northern pike, *Esox lucius*), are not color coded. Sequences are identified by the first letter of the genus and species followed by the last four digits of the NCBI or Ensemble reference gene accession number (see supplementary table S1, Supplementary Material online for a full list of genes).

**Fig. S3. Phylogeny of Actinopterygian HIF $\alpha$  reconstructed by Bayesian inference using amino acid sequences deduced for full length proteins.** Evolutionary analyses were conducted in BEAST 2 (v2.6.1) using a JTT matrix-based model with 6 gamma categories (+G) and allowing for invariants (+I). The tree with maximum clade credibility and mean heights is shown with posterior probability values next to the branches. The highest tree likelihood was -20378.55 with an ESS of 964. The tree was re-rooted on the outgroup for visualization. Four HIF $\alpha$  homology groups are indicated to the right and the following taxa are color coded within each group: Otocephala (green); Salmoniformes (orange); Neoteleostei (blue). The outgroup, *Ciona intestinalis*, basal Actinopterygian (spotted gar, *Lepisosteus oculatus*), basal teleost (Asian arowana, *Scleropages formosus*), and sister taxa to Salmoniformes (Northern pike, *Esox lucius*), are not color coded. Sequences are identified by the first letter of the genus and species followed by the last four digits of the NCBI or Ensemble reference gene accession number (see supplementary table S1, Supplementary Material online for a full list of genes).

**Fig. S4. Phylogeny of Actinopterygian HIF $\alpha$  reconstructed by maximum likelihood using amino acid sequences deduced for full length proteins.** Evolutionary analyses were conducted in MEGAX (v10.1.8) using a JTT matrix-based model with 6 gamma categories (+G) and allowing for invariants (+I). The tree with the highest log likelihood (-20259.51) is shown with

bootstrap values next to the branches. The tree was re-rooted on the outgroup after analysis. Four HIF $\alpha$  homology groups are indicated to the right and the following taxa are color coded within each group: Otocephala (green); Salmoniformes (orange); Neoteleostei (blue). The outgroup, *Ciona intestinalis*, basal Actinopterygian (spotted gar, *Lepisosteus oculatus*), basal teleost (Asian arowana, *Scleropages formosus*), and sister taxa to Salmoniformes (Northern pike, *Esox lucius*), are not color coded. Sequences are identified by the first letter of the genus and species followed by the last four digits of the NCBI or Ensemble reference gene accession number (see supplementary table S1, Supplementary Material online for a full list of genes).

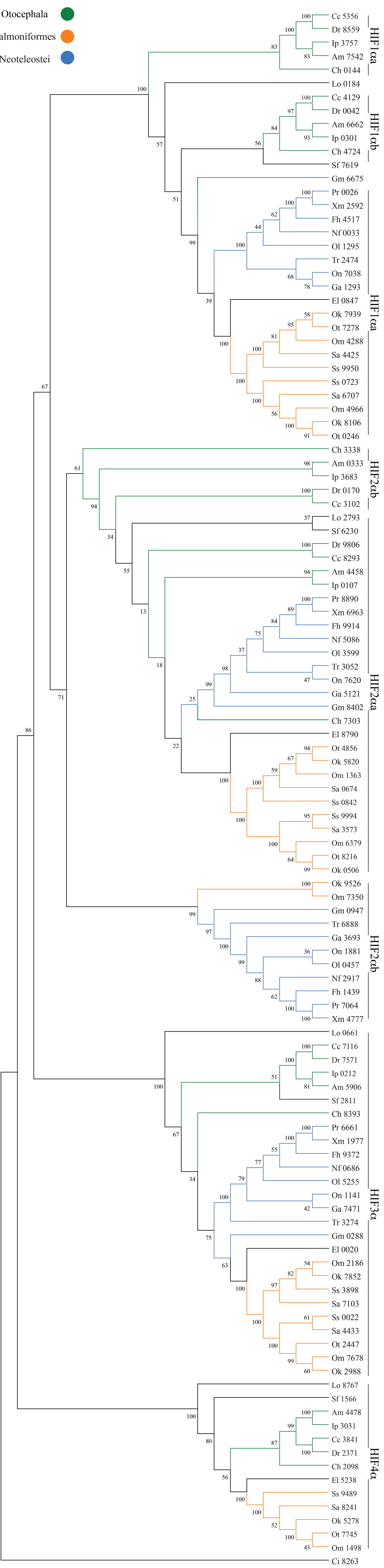
- Otocephala ●
- Salmoniformes ●
- Neoteleostei ●



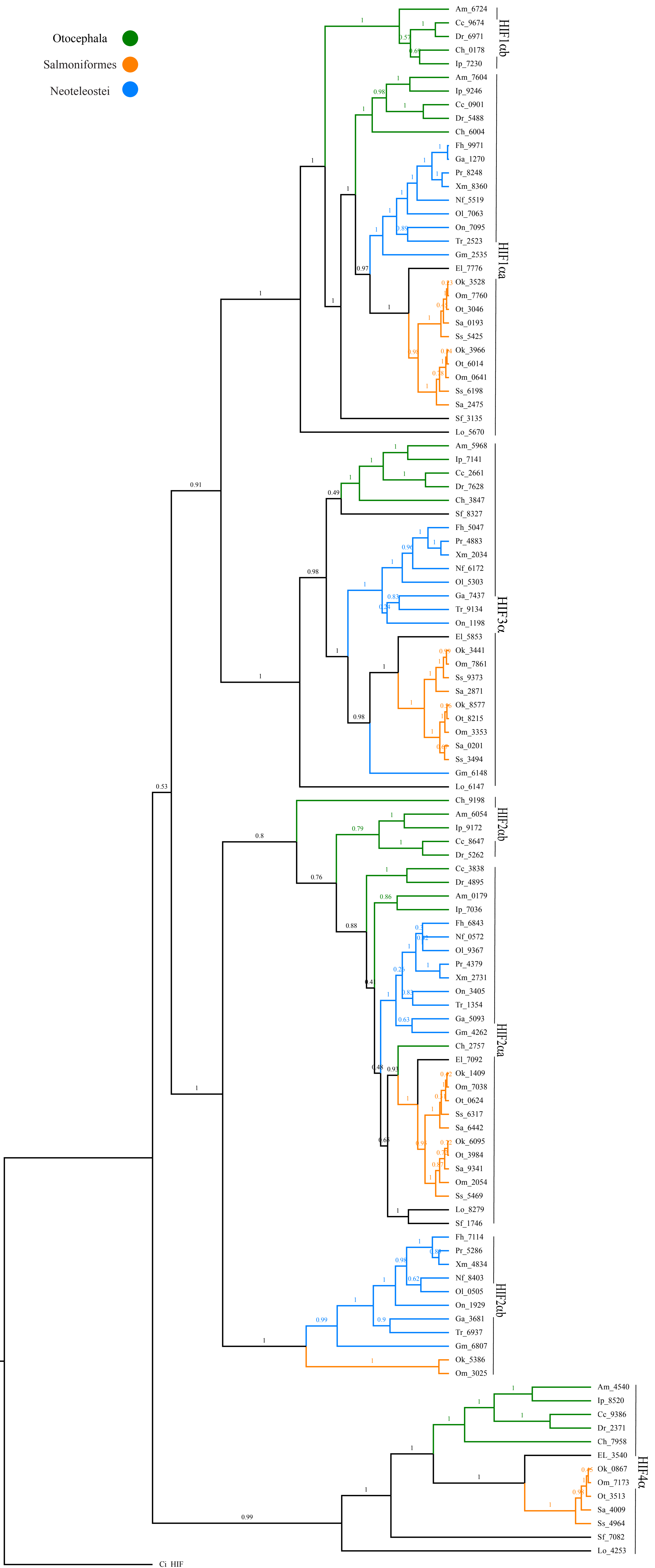
Otocephala ●

Salmoniformes ●

Neoteleostei ●



- Otocephala ●
- Salmoniformes ●
- Neoteleostei ●



- Otocephala ●
- Salmoniformes ●
- Neoteleostei ●

